IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-28. (Cancelled)

28. (Currently amended) Method for extracorporeal manipulation, depletion, and/or removal of soluble, suspended components or cellular blood components comprising the following steps:
    a) Optionall~~y~~ separation of the blood into one or more fractions with solid and/or liquid components;
    b) Binding of soluble, suspended, or cellular blood components of the blood to a surface or particle coupled to a polypeptide ~~according to any one of claims 1 through 18~~ wherein the polypeptide comprises at least three components A and at least two components B, wherein each component A is a monomer of a member of the TNF ligand family or a functional fragment and/or a functional variant thereof, and each component B is a peptide linker; and
    c) Optionall~~y~~ separation of the bound soluble, suspended, or cellular blood components of the blood.

29. (Original) Method according to claim 28, wherein before step a) or b) blood is taken from a patient.

30. (Original) Method according to claim 28, wherein after a step b) or c), the thus treated blood or blood fraction is reinjected into a patient.

31. (New) Method according to claim 28, wherein components A are identical or different.

32. (New) Method according to claim 28, wherein components A stem from the same organism or different organisms.

33 . (New) Method according to claim 28, wherein components A are selected from the group, consisting of FasL, TRAIL, TNF, CD30L, CD40L, OX40L, RANKL,

TWEAKL, LTalpha, LTbeta, LIGHT, CD27L, 41-BB, 41BBL, GITRL, APRIL, EDA, VEGI, and BAFF.

34. (New) Method according to claim 28, wherein components B each link together two of the at least three components A.

35. Method according to claim 28, wherein at least one of components B has the amino acid sequence $(GGGS)_3$ or $(GGGS)_4$.

36. (New) Method according to claim 28, wherein components A and components B form a trimeric protein structure.

37. (New) Method according to claim 36, wherein components A and components B form a homotrimeric protein structure.

38 9. (New) Method according to claim 36, wherein components A and components B form a heterotrimeric protein structure.

39. (New) Method according to claim 28, wherein components B are identical or different.

40. (New) Method according to claim 28, wherein components B stem from the same organism or different organisms.

41. (New) Method according to claim 28, wherein the polypeptide has a preferably N-terminal tag sequence, particularly a His tag sequence or a Flag tag sequence.

42. (New) Method according to claim 28, wherein the polypeptide has a preferably N-terminal leader peptide sequence.

43. Method according to claim 28, wherein the polypeptide has at least one other component C, which is an antibody fragment or a different protein or peptide, which selectively recognizes a specific target molecule on the cell surface.

44. (New) Method according to claim 43, wherein component C is an antibody fragment from a mammal, particularly of murine or human origin, or a humanized antibody fragment.

45. (New) Method according to claim 43, wherein the antibody fragment can be present in different antibody formats, e.g., as scFv, particularly scFv40.

46. (New-withdrawn) Method according to claim 43, wherein component C is a protein or peptide with specificity for a cell surface molecule, particularly a cytokine receptor, a growth factor receptor, an integrin, or cell adhesion molecule.

47. (New-withdrawn) Method according to claim 46, wherein the cytokine receptor is selected from the group of the TNFR gene family.